

Amendments to the Claims:

1 – 20 (cancelled)

21. (new) An isolated embryonic stem (ES) cell, which is an interspecies *Mus musculus* X *Mus spretus* hybrid ES cell.

22. (new) The isolated ES cell according to claim 21, characterised in that said interspecies *Mus musculus* X *Mus spretus* hybrid ES cell has germ line transmission capability.

23. (new) The isolated ES cell according to claim 21, wherein more than 40% of the microsatellites of the DNA of said ES cell are polymorphic in length.

24. (new) The isolated ES cell according to claim 21, wherein more than 70% of the microsatellites of the DNA of said ES cell are polymorphic in length.

25. (new) The isolated ES cell according to claim 21, wherein more than 90% of the microsatellites of the DNA of said ES cell are polymorphic in length.

26. (new) The isolated ES cell according to claim 21,, wherein the genomic background of *Mus spretus* is a from SPRET/Ei (Spain) Ei *Mus spretus* strain mice.

27. (new) The isolated ES cell according to claim 21, wherein the genomic background of *Mus musculus* is from C57BL/6J.

28. (new) The isolated ES cell according to claim 21, wherein said interspecies hybrid

ES cell are derived from SPRET/Ei *Mus spretus* strain x C57BL6/J *Mus musculus* strain.

29. (new) A population of the isolated embryonic stem (ES) cell according to claim 21.

30. (new) A pure population of the isolated embryonic stem (ES) cell according to claim 21.

31. (new) A method for introducing mutations into the *Mus spretus* genome, said method comprising the steps of:

a) transfecting an isolated embryonic stem (ES) cell of claim 22, with a gene-targeting construct, which specifically recombines homologously with said gene in *Mus spretus*,

b) assessing said transfected *Mus musculus* x *Mus spretus* hybrid ES cells for homologous recombination,

c) generating chimeric mice comprising said homologous recombination by blastocyst injection,

d) assessing germline transmission of the *Mus spretus* genome and

e) breeding said chimeric mice, which transmit the *Mus spretus* genome, to homozygosity, in a pure *Mus spretus* background.

32. (new) The method according to claim 31, wherein the mutations are specifically introduced into the *Mus spretus* allele.

33. (new) The method of claim 31, wherein the mutations are selected of the group consisting of null mutations, point mutations, translocations, inversions and deletions.

34. (new) A method for analysing gene function or identification of quantitative trait loci comprising the step of generating radiation-induced chromosomal deletions in the interspecies *Mus musculus* X *Mus spretus* hybrid ES cells of claim 22.
35. (new) A high-throughput analysis system for analysing gene function or identification of quantitative trait loci comprising the isolated interspecies *Mus musculus* X *Mus spretus* hybrid embryonic stem (ES) cell of claim 21, or a population of said stem cell.